

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:16 ; Search time 299.73 Seconds
(without alignments)
24.636 Million cell updates/sec

Title: US-09-331-631A-3_COPY_186_248
Perfect score: 353
Sequence: 1 KRDPQOREYEDCRRCEQOE.....LINPORGSGRYEEGEEKS 63

Scoring table:
BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353	100.0	666	10 Q9SP14	Q9SP14 macadamia i
2	334	94.6	625	10 Q9SP13	Q9SP13 macadamia i
3	332	94.1	666	10 Q9SP15	Q9SP15 macadamia i
4	125.5	35.6	593	10 Q9SEW4	Q9SEW4 juglans reg
5	118.5	33.6	525	10 Q43358	Q43358 theobroma c
6	103	29.2	637	10 Q03678	Q03678 hordeum vul
7	89.5	25.4	810	10 Q92W13	Q92W13 cucurbita m
8	85.5	24.2	1483	5 Q9VD46	Q9VD46 drosophila
9	84	23.8	236	10 Q81254	Q81254 zea mays su
10	82	23.2	630	5 Q9W4J3	Q9W4J3 drosophila
11	81	22.9	242	10 Q81251	Q81251 zea mays su
12	81	22.9	242	10 Q9SBE6	Q9SBE6 zea mays su
13	81	22.9	539	4 Q9NDA2	Q9NDA2 homo sapien
14	80	22.7	238	10 Q81257	Q81257 zea luxurta
15	80	22.7	393	10 Q9ZTP0	Q9ZTP0 oryza sativ
16	79	22.4	238	10 Q81258	Q81258 zea luxurta
17	79	22.4	238	10 Q9SBE5	Q9SBE5 zea luxurta
18	79	22.4	238	10 Q9SBE6	Q9SBE6 zea luxurta
19	79	22.4	242	10 Q81260	Q81260 tripsacum d

20	79	22.4	246	10 Q81261	Q81261 tripsacum d
21	78.5	22.2	1655	5 Q24754	Q24754 drosophila
22	78	22.1	240	10 Q81252	Q81252 zea mays su
23	78	22.1	240	10 Q9SBE0	Q9SBE0 zea mays su
24	78	22.1	240	10 Q9SBE9	Q9SBE9 zea mays su
25	78	22.1	240	10 Q9SBE7	Q9SBE7 zea mays su
26	78	22.1	411	5 P91419	P91419 caenorhabdi
27	78	22.1	540	10 Q03866	Q03866 zea mays (m
28	77	21.8	238	10 Q81255	Q81255 zea mays su
29	76.5	21.7	226	10 Q9S709	Q9S709 arabidopsis
30	76.5	21.7	1128	5 Q9VZ60	Q9VZ60 drosophila
31	75.5	21.4	239	10 Q9SBE1	Q9SBE1 zea mays su
32	75.5	21.4	556	5 Q76940	Q76940 drosophila
33	75.5	21.4	663	5 Q9W352	Q9W352 drosophila
34	75	21.2	562	5 Q9U345	Q9U345 caenorhabdi
35	75	21.2	568	5 Q9U344	Q9U344 caenorhabdi
36	75	21.2	2123	5 Q9U957	Q9U957 dictyostell
37	74.5	21.2	238	10 Q81249	Q81249 zea mays su
38	74.5	21.1	238	10 Q9SBE8	Q9SBE8 zea mays su
39	74.5	21.1	407	10 Q41750	Q41750 zea mays (m
40	74.5	21.1	582	10 Q03865	Q03865 zea mays (m
41	74.5	21.1	686	5 Q45255	Q45255 caenorhabdi
42	74.5	21.1	1309	5 Q9VDE9	Q9VDE9 drosophila
43	74	21.0	236	10 Q81250	Q81250 zea mays su
44	74	21.0	236	10 Q9SBE2	Q9SBE2 zea mays su
45	74	21.0	406	2 Q87306	Q87306 borrelia bu

ALIGNMENTS

RESULT 1
Q9SP14 PRELIMINARY: PRT: 666 AA.
ID Q9SP14;
AC Q9SP14;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUC KERNEL.
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161884; AAD54245.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFM: PF00546; Seedstore-7s; 1.
SQ SEQUENCE 666 AA: 78243 MW: 0ECA22E8710FA7B CRC64;

Query Match 100.0% Score 353; DB 10; Length 666;
Best Local Similarity 100.0% Pred. No. 2.2e-34;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRDPQOREYEDCRRCEQOEPPROYOCCORRCRCEQORH*CGDLINPORGSGRYEEGEE 60
DB 186 KRDPQOREYEDCRRCEQOEPPROYOCCORRCRCEQORH*CGDLINPORGSGRYEEGEE 245
QY 61 KOS 63
DB 246 KOS 248
RESULT 2
Q9SP13

ID	09SPJ3	PRELIMINARY;	PRT;	625 AA.
AC				
DT	01-MAY-2000 (TReMBLrel. 13, Created)			
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)			
DT	01-0CC-2000 (TReMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR (FRAGMENT).			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nult).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Manoilophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI:"taxid=60698;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=NUT KERNEL			
RA	Marcus J.P., Coulter K.C., Green J.L., Manners J.M.;			
RT	"A family of antimicrobial peptides is produced by processing of a 7S			
RL	globulin protein in Macadamia integrifolia."			
DR	Plant J. 0:0-0(1999).			
DR	EMBL; AF161885; AAD54246.1; "-			
DR	HSSP; P02853; 2PHL.			
DR	INTERPRO; IPR001113; "-			
DR	PFAM; PF00546; Seedstore_7s; 1.			
FT	NON_TER			
SQ	SEQUENCE	625 AA;	73586 MW;	415808a89d370296 CRC64;

Query Match	Similarity	Score	DB	Length
Best Local	94.68	334	98	625
Matches	59	Conservative	2	Mismatches
			2	Indels
				Gaps
0Y	1	KRDPOQRETEECRCRCEDEQEPRODTCCQRCRCEQDROHGSGDILINRGSGSGREGE	60	
Db	145	KRDPOQRETEECRCRCEDEQEPRIOTCCQRCQEDROHGSGDILINPDRGSGREGE	204	
0Y	61	KOS	63	
Db	205	KOS	207	

DR	SEQUENCE	666 AA
DR	PFAM; PF00546; Seedstore-7s; 1.	
DR	INTERPRO; IPR001113; -	
DR	HSSP; P02853; 2PHL	
DR	EMBL; AF161883; AAD54244.1; -	
DR	plant J. 0:0-0(1999).	
RL	glutulin protein in Macadamia integrifolia kernels."	
RA	"A family of antimicrobial peptides is produced by processing of a 7s	
RA	Marcus J P., Goulter K.C., Green J.L., Manners J.M.;	
RC	TISSUE-NUT KERNEL;	
RN	SEQUENCE FROM N.A.	
RN	RP	
OX	NCBI_TaxID=60698;	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; Eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)	
DE	VICILIN PRECURSOR.	

Query Match	94.18:	Score 332:	DB 10:	Length 666:
Best Local Similarity	92.18:	Pred. No. 7.3e-37:		
Matches 58:	Conservative 4:	Mismatches 1:	Indels 0:	Gaps
<p> 1 KRDPOREYEDCRRRCRCEOEPRDQYOCORCRCEOQROHGRGGDILNPDGSGGARYEESEE 60 186 KRDPOREYEDCRRRCRCEOEPRDQYOCORCRCEOQROHGRGGDILNPDGSGGARYEESEE 24 ob </p>				

QY	61	KQS	63
		:11	
Db	246	EQS	248

RESULT	4		
09SEM4			
ID	09SEM4	PRELIMINARY;	PRT; 593 AA.
AC	09SEM4;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).		
OS	Juglans regia (English walnut).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC	Fagales; Juglandaceae; Juglans.		
OX	NCBI_TaxID=51240;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-CV. SUNLAND. TISSUE-SOMATIC EMBRYO LINE;		
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;		
RT	"Identification and cloning of a cDNA encoding a vicilin-like protein"		
RT	Jug r 2, from English walnut kernel (Juglans regia) a major food		
RT	allergen."		
RL	Submitted (MAY-1998) to the EMBL/Genbank/DBU databases.		
DR	EMBL; AF066605; AAF18269.1; -		
DR	HSSP; P02853; ZPHL.		
DR	INTERPRO: IPR001113; -		
DR	PFAM; PF00546; Seedstore_7s; 1.		
FT	NON_TER	1	
QO	SEQUENCE	593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;	

	Query Match	Similarity	35.6%	Score	125.5	DB	10	Length	599;
	Best Local	Similarity	45.9%	Pred No.	3.3e-07				
	Matches	Conservative	28;	Mismatches	12;	Indels	5;	Gaps	4
OY	1	KRDPOQREYEDCRRC--EQEPRQOYOQCQRG-RPQQOHGR-GGDLLINPQGSGGYE	56						
		: :	:			:	:	:	
Dd	116	RDDPQ-QYNRCQRQIQIODESPERQDQCQRCEROYKEQGGERGEPASPRESRGREB	174						
OY	57	E 57							
Dd	175	E 175							

RESULT	5		
043358			
ID	043358	PRELIMINARY;	PRT; 525 AA.
AC	043358;		
DT	01-NOV-1996 (TEMBLrel. 01, Created)		
DT	01-NOV-1996 (TEMBLrel. 01, Last sequence update)		
DT	01-OCT-2000 (TEMBLrel. 15, Last annotation update)		
DE	VICILIN PRECURSOR.		
GN	CSV.		
OS	Theobroma cacao (Cacao).		
OC	Euxaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
CC	Magnoliophyta: Eudicotyledons: core eudicots; Rosidae; eurosids II;		
CC	Malvales; Malvaceae; Theobroma.		
OX	NCBI_TaxID=3641;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LEAVES;		
RX	MEDLINE=92288309; Pubmed=1600151;		
RA	McHenry L., Fritz P.J.;		
RT	"Comparison of the structure and nucleotide sequences of vicilin genes		
RT	of cocoa and cotton raise questions about vicilin evolution.";		
RL	Plant Mol. Biol. 18:1173-1176(1992).		
DR	EMBL; X62625; CAA44493.1; -		
DR	EMBL; X62626; CAA44494.1; -		
DR	HSSP; P02853; ZPHL.		

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshfeghi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nyskern D.R., Patel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.C.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylvester R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
DR EMBL: AE003737; AAF55957.1; -
DR FlyBase: FBgn0038932, CG5740.
SQ SEQUENCE 1483 AA: 169708 MW: 370690282EC21B375 CRC64;

Query Match	24.2%;	Score 85.5;	DB 5;	Length 1483;
Best Local Similarity	33.7%;	Pred. No. 0.049;		
Matches 29; Conservative	7;	Mismatches 21;	Indels 29;	Gaps 5

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Oy 1 KRPDQ---REYECRRRCRCEQEPQOYOCRCRCRQQRHG---RGDDLNPQRGGSGR 54
    :||:  ||  : |||||  ||  ||||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 1349 RRPRAEDUREITFLTRCESQ--RDLYVLTDRLRQMQLMSQMNGD-----RKGGGK 1402

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OY      55 -----YEEGEEKOS 63
          ||| ||:|
DB      1403 AVKKPPKSIATSCDVYEENERES 1428

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RESULT		9	
ID	081254		
AC	PRELIMINARY;	PRT;	236 AA.
DT	01-NOV-1998 (TREMBLE)		
DT	01-NOV-1998 (TREMBLE)		08, last sequence update)
DT	01-OCT-2000 (TREMBLE)		15, last annotation update)
DE	GLOBULIN-1 (FRAGMENT).		
OS	Zea mays subsp. parviglumis.		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta		
OX	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	HILLON H., Gaut B.S.;		
RT	"Specification and domestication in maize and its wild relatives:		
RL	evidence from the Globulin-1 gene.";		
DR	EMBL: AF064222; AAC31465.L; -.		
DR	HSPD: P50477; ICAU.		
DR	MENDEL: 31896; Zeama; 1188; 31896.		
DR	INTERPRO: IPR000901; -.		
DR	INTERPRO: IPR001113; -.		
DR	PFAM: PF00546; Seedstore_7s; 1.		
DR	PROSITE: PS00867; CPSSSE_2; UNKNOWN_1.		
FT	NON_TER	236	236
SQ	SEQUENCE	236 AA;	27050 MW; 36A7D94C5213F206 CRC64;

Query Match	23.8%;	Score 84;	DB 10;	Length 236;
Best Local Similarity	35.0%;	Pred. NO. 0.013;		
Matches 21;	Conservative 6;	Mismatches 19;	Indels 14;	Gaps 2

0Y 12 CRRCEQEPPOYQCQRRCREQQRHGRGDLINPQRGSGRYE-----EGEEKQ 62

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      ||||| : ||| : ||| : |||
Db 40 CVRRCEDPRWHQPRCLQEGCREERSRHADD-----RSGEGSSSEDERERKQKEKEKEEK 94

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RESULT 10
Q9W4J3
ID Q9W4J3 PRELIMINARY; PRT; 630 AA

DT	01-MAY-2000	(TREMblrel. 13, Created)
DT	01-MAY-2000	(TREMblrel. 13, Last sequence update)
DT	01-MAY-2000	(TREMblrel. 13, Last annotation update)
DE	CG3546 PROTEIN.	

- OS *Drosophila melanogaster* (Fruit fly).
- OC *Eukaryota*: Metazoa: Arthropoda: Hexapoda: Insecta;
- OC *Pterygota*: Neoptera: Endopterygota: Diptera: Brachycera; Muscomorpha
- OC *Ephyridioidea*; *Drosophilidae*; *Drosophila*.

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RN      [1]
RP      SEQUENCE FROM N.A.
RC
RC      STRAIN=BERKELEY;
RX      MEDLINE=20196006; PubMed=10731132;

```

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.

RA Abdil J.F., Agdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.N.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Chatterjee S., Doolan C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Duggan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlitta S., Fleischman
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlitta S., Fleischman

RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Tallal M., Kalish F., Kanden G.H., Ke Z., Kennison J.A., Ketchum
RA Tallal M., Kalish F., Kanden G.H., Ke Z., Kennison J.A., Ketchum

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mekulov G., Mlshina N.V., Moarry C., Morris J., Mosheli A., Mount S.M., Moy M., Murray I., Murray D., Nelson R.I.

RA Metzger D.R., Nelson R.A., Nixon A., Nussarein U.R., Pacht V.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.
R Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
Cotton E., Crowley A.C., Crowley M., Cresswell D., Cunniff

RA Wang Z.-Y., Wattarman D.A., Weinstein G.M., Weissenbach J.,
RA Svirskas R.S., Vector C., Turner K., Venter E., Wang A.H., Wang X.
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003431; AAF45958.1; -

Query Match 23.2%, Score 82; DB 5; Length 630;

Query Match	23.2%;	Score 82;	DB 5;	Length 630;
Best Local Similarity	45.2%;	Pred. No. 0.056;		
Matches	19;	Conservative 10;	Mismatches 11;	Indels 2;
				Gaps 1

QY 1 KRDPQREYEDCRRR--CEQOEPRQIYOCRCRCREOQRHGR 40
:|:::|:::|:::|:::|
Db 497 RRRPQQQLQQRRRKTKQQQKRRRQQQQQKRRRQQQQQQRR 538

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RESULT 11
081251 PRELIMINARY; PRT; 242 AA.
AC 081251:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. mays (maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=4578;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL; AF064214; AAC31457.1; -.
DR HSSP; P50477; 1CAU.
DR MENDEL; 31893; Zeama.1188; 31893.
DR INTERPRO; IPR000901; -.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 27860 MW; 913912DE924B0ADB CRC64;

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Query Match 22.9%; Score 81; DB 10; Length 242;
 Best Local Similarity 35.9%; Pred. No. 0.03;
 Matches 23; Conservative 7; Mismatches 18; Indels 16; Gaps 3;

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OY 12 CRRCE---QOEPRQOYOCORCRCEQORHGRGDLINPORGSG-----RYEEG 58
      |||||  |||  |||::||::||  |||  |||  |||
Db 40 CVRCEPRPMHQRPCLEQCRERERKRGHE---TDRSGSGSSDEDERERERQEK 96
OY 59 EEKQ 62
      |||||
Db 97 EEKQ 100

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RESULT 12
09SBE6 PRELIMINARY; PRT; 242 AA.
ID 09SBE6:
AC 09SBE6:
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviflumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL; AF064225; AAC31468.1; -.
DR HSSP; P50477; 1CAU.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 27856 MW; 8E6DB2C9E45C6BAD CRC64;

```

Query Match 22.9%; Score 81; DB 10; Length 242;
 Best Local Similarity 35.9%; Pred. No. 0.03;
 Matches 23; Conservative 7; Mismatches 18; Indels 16; Gaps 3;

```

OY 12 CRRCE---QOEPRQOYOCORCRCEQORHGRGDLINPORGSG-----RYEEG 58
      |||||  |||  |||::||::||  |||  |||  |||
Db 40 CVRCEPRPMHQRPCLEQCRERERKRGHE---TDRSGSGSSDEDERERERQEK 96
OY 59 EEKQ 62
      |||||
Db 97 EEKQ 100

```

```

RESULT 13
09NUA2 PRELIMINARY; PRT; 539 AA.
ID 09NUA2:
AC 09NUA2:
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE DJ0804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
DE (FRAGMENT).
GN AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman J.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049564; CAB87955.1; -.
KW Receptor.
FT NON_TER 539 539
SQ SEQUENCE 539 AA; 55444 MW; AB493953B89D869F CRC64;

```

Query Match 22.9%; Score 81; DB 4; Length 539;
 Best Local Similarity 32.8%; Pred. No. 0.064;
 Matches 19; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

```

OY 5 QOREYEDCRRRCQOEPRQOYOCORCRCEQORHGRGDLINPORGSGRYEEGEEKO 62
      ||:::  ::|||  |||  |||  |||  |||  |||  |||  |||  |||
Db 58 QQQQQQQQQQQQQQQQQQQQQQQQETSPRQQQQQGGEDGSPQAHRRGPTGYLVDEEQ 115

```

```

RESULT 14
081257 PRELIMINARY; PRT; 238 AA.
ID 081257:
AC 081257:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea luxurians (Teosinte).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=15945;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL; AF064228; AAC31471.1; -.
DR HSSP; P50477; 1CAU.
DR MENDEL; 31899; Zealu.1188; 31899.
DR INTERPRO; IPR000901; -.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 27233 MW; FD31A80666738E68 CRC64;

```

Query Match 22.7%; Score 80; DB 10; Length 238;
 Best Local Similarity 35.5%; Pred. No. 0.039;

Matches	22; Conservative	6; Mismatches	18; Indels	16; Gaps	3; Ambiguous
OY	12	CARRRCEQOEPRROVYCCORCRE-----OQROHGRGGLINQNGSGS-----RYEEGEE	60	12	11
	1		1		4
	1		1		4
Db	40	CVRREDPRMWRSMRSCLDCCRRERERERKQERSRHHAD-----RSGEGSGSEDERDQEKTE	94	12	11
	1		1		4
OY	61	KQ	62	11	11
	1		1		4
Db	95	KQ	96	11	11
	1		1		4

RESULT 15

ID	09ZTP0	PRELIMINARY;	PRT:	393 AA.
AC	09ZTP0;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	HYPOTHETICAL 45.3 KDA PROTEIN.			
GN	OSE705.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.			
OC				
OX	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=LOMELLO;			
RA	Chen P.W., Chen L.J.;			
RL	Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF049348; ADD02494.1; -.			
KR	Hypothetical protein			
SO	SEQUENCE 393 AA; 45258 MM; DBD01934BA2F9E95 CRC64;			

```
Search completed: March 1, 2001, 16:09:17
Job time: 1561 sec
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